IN THE CLAIMS

Claims 124-150 are pending in the present application. The following is the status of the claims of the above-captioned application, as amended.:

Claims 1-123 cancelled.

124. (Currently Amended) A method for producing a secreted heterologous polypeptide, comprising:

(a) cultivating a mutant cell of a parent *Fusarium venenatum* cell under conditions conducive for the production of the secreted heterologous polypeptide, wherein (i) the mutant cell comprises a first nucleic acid ~~sequence~~ encoding the secreted heterologous polypeptide, and (ii) the mutant cell comprises a second nucleic acid ~~sequence~~ which comprises a ~~modification~~ disruption or a deletion ~~of~~ in a cyclohexadepsipeptide synthetase gene, wherein the mutant cell produces less cyclohexadepsipeptide than the parent *Fusarium venenatum* cell when cultured under the same conditions as a result of the disruption or the deletion in the cyclohexadepsipeptide synthetase gene; and

(b) isolating the secreted heterologous polypeptide from the cultivation medium.

125. (Previously Presented) The method of claim 124, wherein the *Fusarium venenatum* cell is *Fusarium venenatum* ATCC 20334.

126. (Previously Presented) The method of claim 124, wherein the *Fusarium venenatum* cell is a morphological mutant.

127. (Previously Presented) The method of claim 126, wherein the *Fusarium venenatum* cell is a morphological mutant of *Fusarium venenatum* ATCC 20334.

128. (Currently Amended) The method of claim 124, wherein the cyclohexadepsipeptide synthetase gene encodes a cyclohexadepsipeptide synthetase selected from the group consisting of:

(a) a cyclohexadepsipeptide synthetase having an amino acid sequence which has at least 70% identity with SEQ ID NO: 2; and

(b) a cyclohexadepsipeptide synthetase which is encoded by a nucleic acid ~~sequence~~ which hybridizes under at least medium stringency conditions with (i) the nucleic acid

~~sequence~~ of SEQ ID NO: 1, (ii) the cDNA ~~sequence~~ of SEQ ID NO: 1, or (iii) a complete complementary strand of (i)~~,~~ or (ii) ~~, or (iii)~~, wherein medium stringency conditions are defined as prehybridization and hybridization at 45°C in 5X SSPE, 0.3% SDS, 200 µg/ml sheared and denatured salmon sperm DNA, and 35% formamide and washing three times each for 15 minutes using 2X SSC, 0.2% SDS at 55°C~~; and~~

~~(c) a fragment of (a) or (b) that has cyclohexadepsipeptide synthetase activity~~.

129. (Previously Presented) The method of claim 124, wherein the cyclohexadepsipeptide synthetase gene encodes the cyclohexadepsipeptide synthetase of SEQ ID NO: 2.

130. (Previously Presented) The method of claim 129, wherein the cyclohexadepsipeptide synthetase gene has the nucleic acid sequence of SEQ ID NO: 1.

131. (Currently Amended) The method of claim 124, wherein the mutant cell produces at least ~~about~~ 25% less of the cyclohexadepsipeptide than the parent ~~filamentous fungal~~ *Fusarium venenatum* cell when cultured under identical conditions.

132. (Previously Presented) The method of claim 124, wherein the mutant cell produces no cyclohexadepsipeptide.

133. (Currently Amended) The method of claim 124, wherein the mutant cell comprises at least two copies of the first nucleic acid ~~sequence~~.

134. (Previously Presented) The method of claim 124, wherein the secreted heterologous polypeptide is a hormone, enzyme, receptor or portion thereof, antibody or portion thereof, or reporter.

135. (Previously Presented) The method of claim 134, wherein the enzyme is an oxidoreductase, transferase, hydrolase, lyase, isomerase, or ligase.

136. (Currently Amended) The method of claim 124, wherein the mutant cell further comprises one or more ~~third~~ nucleic acids ~~sequences~~, in addition to the two nucleic acids already present in the mutant cell, which ~~have been modified~~ comprise a disruption or a deletion to reduce or eliminate expression of the one or more ~~third~~ additional nucleic acids ~~sequences~~.

137. (Currently Amended) The method of claim 136, wherein ~~the~~ a third nucleic acid ~~sequence~~ encodes an enzyme selected from the group consisting of an aminopeptidase, amylase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase, beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase, invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme, ribonuclease, transglutaminase, and xylanase.

138. (Currently Amended) The method of claim 136, wherein ~~the~~ a third nucleic acid ~~sequence~~ encodes a protease.

139. (Currently Amended) A cyclohexadepsipeptide-deficient mutant cell of a parent *Fusarium venenatum* cell, comprising (i) a first nucleic acid ~~sequence~~ encoding a secreted heterologous polypeptide, and (ii) a second nucleic acid ~~sequence~~ comprising a ~~modification~~ disruption or a deletion ~~of~~ in a cyclohexadepsipeptide synthetase gene, wherein the *Fusarium venenatum* mutant cell produces less cyclohexadepsipeptide than the parent *Fusarium venenatum* cell when cultured under the same conditions as a result of the disruption or the deletion in the cyclohexadepsipeptide synthetase gene.

140. (Previously Presented) The mutant cell of claim 139, wherein the *Fusarium venenatum* cell is *Fusarium venenatum* ATCC 20334.

141. (Previously Presented) The mutant cell of claim 139, wherein the *Fusarium venenatum* cell is a morphological mutant.

142. (Previously Presented) The mutant cell of claim 141, wherein the *Fusarium venenatum* cell is a morphological mutant of *Fusarium venenatum* ATCC 20334.

143. (Currently Amended) The mutant cell of claim 139, wherein the cyclohexadepsipeptide synthetase gene encodes a cyclohexadepsipeptide synthetase selected from the group consisting of:

(a) a cyclohexadepsipeptide synthetase having an amino acid sequence which has at least 70% identity with SEQ ID NO: 2; and

(b) a cyclohexadepsipeptide synthetase which is encoded by a nucleic acid ~~sequence~~ which hybridizes under at least medium stringency conditions with (i) the nucleic acid ~~sequence~~ of SEQ ID NO: 1, (ii) the cDNA ~~sequence~~ of SEQ ID NO: 1, or (iii) a complete complementary strand of (i)~~,~~ or (ii) ~~, or (iii)~~, wherein medium stringency conditions are defined as prehybridization and hybridization at 45°C in 5X SSPE, 0.3% SDS, 200 µg/ml sheared and denatured salmon sperm DNA, and 35% formamide and washing three times each for 15 minutes using 2X SSC, 0.2% SDS at 55°C ~~; and~~

~~(c) a fragment of (a) or (b) that has cyclohexadepsipeptide synthetase activity~~.

144. (Previously Presented) The mutant cell of claim 139, wherein the cyclohexadepsipeptide synthetase gene encodes the cyclohexadepsipeptide synthetase of SEQ ID NO: 2.

145. (Previously Presented) The mutant cell of claim 144, wherein the cyclohexadepsipeptide synthetase gene has the nucleic acid sequence of SEQ ID NO: 1.

146. (Currently Amended) The mutant cell of claim 139, which ~~wherein the *Fusarium venenatum* cell~~ comprises at least two copies of the first nucleic acid ~~sequence~~.

147. (Previously Presented) The mutant cell of claim 139, wherein the secreted heterologous polypeptide is a hormone, enzyme, receptor or portion thereof, antibody or portion thereof, or reporter.

148. (Previously Presented) The mutant cell of claim 147, wherein the enzyme is an oxidoreductase, transferase, hydrolase, lyase, isomerase, or ligase.

149. (Currently Amended) The mutant cell of claim 139, wherein the mutant cell further comprises one or more ~~third~~ nucleic acids ~~sequences~~, in addition to the two nucleic acids already present in the mutant cell, which ~~have been modified~~ comprise a disruption or a deletion to reduce or eliminate expression of the one or more ~~third~~ additional nucleic acids ~~sequences~~.

150. (Currently Amended) The mutant cell of claim 149, wherein ~~the~~ a third nucleic acid ~~sequence~~ encodes an enzyme selected from the group consisting of an aminopeptidase, amylase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase, beta-galactosidase,

glucoamylase, alpha-glucosidase, beta-glucosidase, invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme, ribonuclease, transglutaminase, and xylanase.